

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 7, 2005, 07:04:17 ; Search time 20.4798 Seconds  
(without alignments)  
1193.323 Million cell updates/sec

Title: US-09-939-537-33

Perfect score: 1385

Sequence: 1 BKSCDKHTPCPCPAPBLL.....DETCAPAGQDGLDGLWTTPD 254

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1258	90.8	330	1 GHNU	Ig gamma-1 chain C
2	1252	90.4	374	2 S69339	Ig heavy chain V r
3	1250	90.3	255	4 S31866	Ig gamma-1 chain C
4	1210	87.4	234	2 PT0207	Ig gamma chain C r
5	1171	84.5	377	2 A23511	Ig gamma-3 chain C
6	1169	84.4	377	2 A60764	Ig gamma-3 chain C
7	1151	83.1	289	1 G3HWTI	Ig gamma-3 heavy C
8	1140	82.3	326	1 G2HU	Ig gamma-2 chain C
9	1130	81.6	327	1 G4HU	Ig gamma-4 chain C
10	938.5	67.8	398	1 G3MSM	Ig gamma-3 chain C
11	931.5	67.3	393	1 G3MSM	Ig gamma-1 chain C
12	916	66.1	323	1 GHRP	Ig gamma chain C r
13	905	65.3	399	1 G2MSAM	Ig gamma-2a chain
14	901.5	65.1	328	2 I47160	Ig gamma 2b chain
15	901.5	65.1	328	2 I47159	Ig gamma 2a chain
16	898	64.8	277	2 I47162	Ig gamma 4 chain c
17	896	64.7	329	1 G2GP	Ig gamma-2 chain c
18	880.5	63.6	328	2 I47158	Ig gamma 1 chain c
19	873.5	63.1	328	2 I47161	Ig gamma 3 chain c
20	870.5	62.9	405	1 G2MSBM	Ig gamma-2b chain
21	851	61.4	470	2 S22080	Ig heavy chain pre
22	842.5	60.8	308	2 C30554	Ig heavy chain C r
23	842.5	60.8	472	2 S31459	Ig gamma-1 chain -
24	840.5	60.7	329	1 G3MSC	Ig gamma-3 chain c
25	837	60.4	333	2 PS0018	Ig gamma-2b chain
26	827.5	59.7	444	2 PC4436	monoclonal antibod
27	817.5	59.0	324	1 G1MS	Ig gamma-1 chain C
28	817.5	59.0	326	2 PS0017	Ig gamma-1 chain C
29	804.5	58.1	329	2 S00847	Ig gamma-2c chain

30	804	58.1	330	1 G2MSA	Ig gamma-2a chain
31	804	58.1	469	2 S37483	Ig gamma-2a chain
32	800	57.8	335	1 G2MSAB	Ig gamma-2a chain
33	794	57.3	446	2 S40295	Ig gamma-2a chain
34	780.5	56.4	322	2 PS0019	Ig gamma-2a chain
35	774.5	55.9	474	1 G2MS11	Ig gamma-2b chain
36	759	54.8	327	2 S06611	Ig gamma-2 chain C
37	754.5	54.5	475	2 S01321	Ig gamma heavy cha
38	702	50.7	180	2 I46732	Ig gamma heavy cha
39	574.5	41.5	218	2 A36040	Ig heavy chain V-I
40	572.5	41.3	249	2 S69340	Ig heavy chain VHI
41	566	40.9	152	2 S14236	Ig gamma-1 chain C
42	390.5	28.2	572	2 B46529	Ig y heavy chain (
43	363.5	26.2	476	1 MHMSM	Ig mu chain C regi
44	359	25.9	549	2 S04845	Ig heavy chain pre
45	357.5	25.8	627	2 S14683	Ig mu chain precu

#### ALIGNMENTS

##### RESULT 1

GHNU  
Ig gamma-1 chain C region - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004  
C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146  
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.  
Nucleic Acids Res. 10, 4071-4079, 1982  
A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.  
A:Reference number: A93433; WUID:82274238; PMID:6287432  
A:Accession: A93433  
A:Molecule type: DNA  
A:Residues: 1-330 <ELL>  
A:Cross-references: UNIPROT:P01857; EMBL:Z17370  
A>Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers, ;  
A>Note: Lys-330 is removed after translation  
R:Harris, L.J.  
submitted to the EMBL Data Library, October 1992  
A:Reference number: S33904  
A:Accession: S36861  
A:Molecule type: DNA  
A:Residues: 2-330 <HAR>  
A:Cross-references: EMBL:Z17370  
R:Takahashi, N.; Ueda, S.; Obata, M.; Nakai, S.; Honjo, T.  
Cell 29, 671-679, 1982  
A>Title: Structure of human immunoglobulin gamma genes: implications for evolution of a  
A:Reference number: S33887; WUID:83001943; PMID:6811139  
A:Accession: S33887  
A:Molecule type: DNA  
A:Residues: 88-113;235-330 <TAK>  
A:Cross-references: EMBL:Z17370  
R:Cunningham, B.A.; Rutschauer, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C  
Biochemistry 9, 3161-3170, 1970  
A>Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen  
A:Reference number: A90564; WUID:71064024; PMID:5489771  
A:Contents: myeloma protein Bu  
A:Accession: B90563  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-135 <GUN>  
A>Note: this sequence has the Gln(3) marker, 97-Arg  
R:Rutschauer, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.  
Biochemistry 9, 3171-3181, 1970  
A>Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer  
A:Reference number: A90564; WUID:71064025; PMID:5530842  
A:Contents: Bu  
A:Accession: A90564  
A:Molecule type: protein  
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, '  
A>Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met  
R:Ponstingl, H.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976  
A>Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1e),

Igen Primaerstruktur.  
A/Reference number: A91668; MUID:77070269; PMID:826475  
A/Contents: myeloma protein Nie  
A/Accession: B91668  
A/Molecule type: protein  
A/Residues: 1-34, 'Q', '36-96', 'K', '98-115', 'Q', '117-197', 'D', '199-238', 'D', '240', 'L', '242-268', 'E', '27  
A/Note: This sequence has the Gln(17) and Gln(1) markers  
R/Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1963  
A/Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOL  
A/Reference number: A91723; MUID:83289131; PMID:6884994  
A/Contents: myeloma protein KOL; disulfide bonds  
A/Accession: A91723  
A/Molecule type: protein  
A/Residues: 1-96, 'R', '98-197', 'D', '199-238', 'E', '240', 'W', '242-266', 'D', '268-271', 'D', '273-330' <SCH  
R/Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A/Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A/Reference number: A90665; MUID:71064027; PMID:4923144  
A/Contents: annotation; disulfide bonds  
R/Dreker, U.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A/Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
embromide cleavage products, and the disulfide bridges.  
A/Reference number: A91667; MUID:77070267; PMID:1002129  
A/Contents: annotation; disulfide bonds  
C/Genetics:  
A/Gene: GDB:IGHG1  
A/Cross-references: GDB:120085; OMIM:147100  
A/Map position: 14q32.33-14q32.33  
A/Intons: 99/1; 114/1; 224/1  
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
F/20-85/Domain: immunoglobulin homology <IM1>  
F/137-206/Domain: immunoglobulin homology <IM2>  
F/243-310/Domain: immunoglobulin homology <IM3>  
F/27-83, 144-204, 250-308/Disulfide bonds: #status experimental  
F/103/Disulfide bonds: interchain (to light chain) #status experimental  
F/109, 112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F/180/Binding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 90.8%; Score 1258; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 4, 1e-88;  
Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
Db 99 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 158  
QY 61 NMVYDGEVHNAKTRPEEQYNSTYRVVSLTVLHODMLNGKEYCKVSKNKAAPAPIEKT 120  
Db 159 NMVYDGEVHNAKTRPEEQYNSTYRVVSLTVLHODMLNGKEYCKVSKNKAAPAPIEKT 218  
QY 121 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 180  
Db 219 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 278  
QY 181 PVLDSGSPFLYSKLTVDKSRMQGNVFCSSVMEALAHNYTKQKSLSLSPG 231  
Db 279 PVLDSGSPFLYSKLTVDKSRMQGNVFCSSVMEALAHNYTKQKSLSLSPG 329

RESULT 2  
S69339  
19 heavy chain V region precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C/Accession: S69339; S72664  
R/Thamlich, A.A.; Auccurtier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995

A/Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A/Reference number: S69339; MUID:95262687; PMID:7744049  
A/Accession: S69339  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-374 <KHA>  
A/Cross-references: EMBL:X81695  
R/Thamlich, A.A.  
submitted to the EMBL Data Library, September 1994  
A/Reference number: S72664  
A/Accession: S72664  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-140, 'C', '142-374' <KHA>  
A/Cross-references: EMBL:X81695  
C/Superfamily: immunoglobulin C region; immunoglobulin homology  
Query Match 90.4%; Score 1252; DB 2; Length 374;  
Best Local Similarity 99.1%; Pred. No. 1, 4e-87;  
Matches 229; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
Db 143 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 202  
QY 61 NMVYDGEVHNAKTRPEEQYNSTYRVVSLTVLHODMLNGKEYCKVSKNKAAPAPIEKT 120  
Db 203 NMVYDGEVHNAKTRPEEQYNSTYRVVSLTVLHODMLNGKEYCKVSKNKAAPAPIEKT 262  
QY 121 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 180  
Db 263 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 322  
QY 181 PVLDSGSPFLYSKLTVDKSRMQGNVFCSSVMEALAHNYTKQKSLSLSPG 231  
Db 323 PVLDSGSPFLYSKLTVDKSRMQGNVFCSSVMEALAHNYTKQKSLSLSPG 373

RESULT 3  
S31866  
Ig gamma-1 chain C region - synthetic  
C/Species: synthetic  
A/Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C/Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C/Accession: S31866  
R/Filipula, D.  
submitted to the EMBL Data Library, February 1993  
A/Description: Screening method for protein-protein interactions of cloned gene products.  
A/Reference number: S31866  
A/Accession: S31866  
A/Molecule type: mRNA  
A/Residues: 1-255 <FIL>  
A/Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069  
F/1-32/Region: immunoglobulin  
F/23-255/Region: Escherichia coli outer membrane protein A precursor  
Query Match 90.3%; Score 1250; DB 4; Length 255;  
Best Local Similarity 99.6%; Pred. No. 1, 2e-87;  
Matches 230; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
Db 24 EPKSCDKHTCPCPAPPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVDVSHEDPEVKF 83  
QY 61 NMVYDGEVHNAKTRPEEQYNSTYRVVSLTVLHODMLNGKEYCKVSKNKAAPAPIEKT 120  
Db 84 NMVYDGEVHNAKTRPEEQYNSTYRVVSLTVLHODMLNGKEYCKVSKNKAAPAPIEKT 143  
QY 121 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 180  
Db 144 ISKAGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTP 203

**Oy**        181 PVLSDSGSFLYSKLTVDKSRMQGVFSCSVNHEALNNHYTQKSLSPG 231  
           |||||  
**Dd**        204 PVLSDSGSFLYSKLTVDKSRMQGNVFSCSVNHENLNHNYTQKSLSPG 254

**RESULT 4**

```

Ig gamma chain C region - chimpanzee
C/Species: Pan troglodytes (chimpanzee)
C/Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C/Accession: PTO207
R/Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28: 319-322, 1991
A/Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A/Reference number: PTO207; MUID:91287716; PMID:206315
A/Accession: PTO207
A/Molecule type: mRNA
A/Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: immunoglobulin
C/48-117/Domain: immunoglobulin homology <IMM>

```

```
Query Match      87.4%   Score 1210; DB 2;   length 234;
Best Local Similarity 98.7%   Pred. No. 1.2e-84;
Matches 222; Conservative 1; Mismatches 2; Gaps 0;
```

Qy	1	PPKSCDKNHTGCPRCAPARELLGGSPVFLPPKPKDITLMIERTPEVTCVVVDVSHEDDEVKR	60
Db	10	EPKSCDITHTGCPRCAPARELLGGSPVFLPPKPKDITLMIERTPEVTCVVVDVSHEDDEVKR	69
Qy	61	NMYYDGVENVNAKTKPRREQVNSTYRNVSVLTLYLHDMYLNKGKCYKCVSNKALPAIEIKT	120
Db	70	NMYYDGVENVNAKTKPRREQVNSTYRNVSVLTLYLHDMYLNKGKCYKCVSNKALPAIEIKT	129
Qy	121	ISKAKGQRPREPOVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTT	180
Db	130	ISKAKGQRPREPOVYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTTT	189
Qy	181	PVLSDSGSFPLYSKLTVDKSRKQGGNVSCSMVNEHLYLNHNHYTKS	225
Db	190	PVLSDSGSFPLYSKLTVDKSRKQGGNVSCSMVNEHLYLNHNHYTKS	234

## RESULT 5

IG gamma-3 chain C region (allotype G3m(b) ) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 28-Dec-1987 #sequence\_revision 28-Dec-1987 #text\_change 23-Jul-1999  
 C:Accession: A23511  
 R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.  
 Nucleic Acids Res. 14, 1779-1789, 1986  
 A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cDNA  
 A:Reference number: A23511; MUID:86148507; PMID:3081877  
 A:Accession: A23511  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HUC>  
 A:Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CAA27268.1; PID:g5770556  
 C:Genetics:  
 A:Gene: GDB:IGHG3  
 A:Cross-references: GDB:119339; OMIM:147120  
 A:Map position: 14q32.33-14q32.33  
 A:Intons: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3  
 C:Superfamily: Immunoglobulin C region; immunoglobulin homology  
 C:Keywords: Immunoglobulin  
 C:20-85/Domain: immunoglobulin homology <IMM>

Query Match	84.5%	Score 1171	DB 2	Length 377
Best Local Similarity	92.6%	Pred. 1.9e-81		
Matches 214	Conservative	8	Mismatches 9	Indels 0
			Gaps 0	

  

QY	1	EPKSCDKTHTPPCPAPRLGGSVFLEPPPKXTLMTSRPEVTCVVVDYSHEDPEYK	60
		.....	
Db	146	EPKSCDTPPPCPAPRLGGSVFLEPPPKXTLMTSRPEVTCVVVDYSHEDPEYK	205

Qy	61	NMYVDGVEYHNAKTRPREEOYNSTRVSVYLTVLHODMLNKEKYEKCVSNKALPAPIEKT	120
Db	206	KMYVDGVEYHNAKTRPREEOYNSTRVSVYLTVLHODMLNKEKYEKCVSNKALPAPIEKT	265

```
0Y      121 ISKAKGPREPOVTLPPSDELTKNQVSLTCLVKGFYPSIAIIVEHNSNGPGENNYKTTP 180
```

```
QY      181 PVLSDSGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPG 231
      |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      326 PMUDDSGSFFLYSKLTVDKSRWQGNIFSCSVMEALHNRFYQKSLSLSPG 376
```

## RESULT 6

Ig gamma-3 chain C region, form LAT - human  
 C:Species: Homo sapiens (man)  
 C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
 C:Accession: A60764  
 R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
 Immunogenetics 30, 250-257, 1989  
 A:Title: A human immunoglobulin IGH3 allele (Gmb0, b1, c3, c5, u) with an  
 A:Reference number: A60764; WUID:90007613; PMID:2571587  
 A:Accession: A60764  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-377 <HUC>  
 A:Cross-references: UNIPROT:Q6N4V9  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: immunoglobulin  
 P:20-85/Domain: immunoglobulin homology <IM>

Query Match	84.4%	Score 1169	DB 2	Length 377
Best Local Similarly	92.6%	Pred. No. 2.7e-81		
Matches 114	Conservative	8	Mismatches 9	Indels 0
				Gaps 0

QY	1	EPKSCDKTHTCPCPAPBELLGGSPSFLPPPKKDTLMTSRTEBYTCVVVDVSHEDPEVK	60
Db	146	EPKSCDTRPPRCPCAPBELLGGSPSFLPPPKKDTLMTSRTEBYTCVVVDVSHEDPEVQF	205
QY	61	NMYVDGVEVHNAKTPREBEQYNSTRVSVLTVLVHODMLNGREYKCKVSNKALPAPIEKT	120
Db	206	KMYVDGVEVHNAKTPREBEQYNSTRVSVLTVLVHODMLNGREYKCKVSNKALPAIEKT	255
QY	121	ISKAKGQREPOVYTLPPSRDELITKNVSLTCLVNGFYPSDIAVEMWNSGQEPENNYKTP	180
Db	266	ISKTKGQREPOVYTLPPSRBEEMITKNVSLTCLVNGFYPSDIAVEMWNSGQEPENNYTTP	325
QY	181	PVLDSDSGFPLYSKLTIVDKSRKQCEENVSCSYMHEDLHNHYFOKSLSLSPG	231
Db	326	PVLDSDSGFPLYSRLTIVDKSRKQCEENVSCSYMHEDLHNRFOKSLSLSPG	376

## RESULT 7

I9 gamma-3 heavy chain disease proteins - human  
 CSpecies: Homo sapiens (man)  
 CDate: 31-Dec-1979 #sequence\_revision 23-Oct-1981 #ext\_change 16-Jul-1999  
 CAccession: A50442; A92219; A90198; A93915; A02119  
 R;Frangione, B.; Rosenwasser, E.; Prell, F.; Franklin, E.C.  
 Biochemistry 19, 4304-4308, 1980  
 A>Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-chain  
 A;Reference number: A50442; MUID:81021548; PMID:6774747  
 A;Contents: heavy chain disease protein Wis  
 A;Accession: A50442  
 A;Molecule type: protein  
 A;Residues: 1-289 <FR>  
 A;Note: the molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain  
 A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 con  
 A;Note: the sequence of residues 42-76 was taken from the reference that follows  
 R;Michaelson, T.E.; Frangione, B.; Franklin, E.C.  
 J. Biol. Chem. 252, 883-889, 1977

A>Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication  
A:Reference number: A92219; MUID:77118561; PMID:403363  
A:Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W  
A:Accession: A92219  
A:Molecule type: protein  
A:Residues: 12-97 <MIC>  
A>Note: the hinge region in gamma-3 chains is about four times as long as in other gamma  
idue segment (12-28)  
A>Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter  
R:Moldstein-Rodel, C.; Frangione, B.; Prell, F.; Franklin, E.C.  
Biochem. Biophys. Res. Commun. 71, 1976  
A>Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the  
A:Reference number: A90194; MUID:77021516; PMID:823945  
A:Contents: heavy chain disease protein ZUC, partial sequence corresponding to residues  
A:Accession: A90198  
A:Molecule type: protein  
A:Residues: 59-125, 'EB', 128-226, 228-289 <MOI>  
A>Note: this protein lacks most of the V region, all of the CH1 region, and part of the  
R:Alexander, A.; Steinmetz, M.; Barillet, D.; Frangione, B.; Franklin, E.C.; Hood, L.;  
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
A>Title: gamma heavy chain disease in man: CDNA sequence supports partial gene deletion  
A:Reference number: A93915; MUID:62247835; PMID:680505  
A:Contents: heavy chain disease protein Cmm  
A:Accession: A93915  
A:Molecule type: mRNA  
A:Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
A>Note: a carboxyl-terminal lys is removed posttranslationally  
A>Note: this sequence may represent an allelic form or another gamma chain subclass  
C:Comment: The heavy chain disease protein wis is shown.  
C:Genetics:  
A:Gene: GDB:IGHG3  
A:Cross-references: GDB:119339; OMIM:147120  
A:Map position: 14q32.33-14q32.33  
C:Superfamily: immunoglobulin C region; immunoglobulin; pyroglyutamic acid  
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid  
F:203-270/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:6.140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 83.1%; Score 1151; DB 1; Length 289;  
Best Local Similarity 90.5%; Pred. No. 4.5e-80;  
Matches 209; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 EPKSCDKHTHTPCPCAPAPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 60  
DB 59 EPKSCDTPPCPCPCAPAPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 118  
QY 61 NWYVDGVEVNAKTKPREEQYNSTYRVVSVLTVLDHQMILNGKEYKCKVSNKALPAPIEKT 120  
DB 119 KMYVDGVEVNAKTKPREEQYNSTYRVVSVLTVLDHQMILNGKEYKCKVSNKALPAPIEKT 178  
QY 121 ISKAKGPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGENNYKTTTP 180  
DB 179 ISKTKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGENNYKTTTP 238  
QY 181 PVLDSDGSFELYKLTVDKSRQOGNVPFSCVNHKALHNHYTQKSLSLSPG 231  
DB 239 PMLDSDGSFELYKLTVDKSRQOGNVPFSCVNHKALHNHYTQKSLSLSPG 289

RESULT 8  
GHD  
Ig gamma-2 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004  
C:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A>Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A:Reference number: A93906; MUID:82197621; PMID:6804948  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <ELL>

A:Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; P  
A>Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and fu  
A:Reference number: A92809; MUID:81007873; PMID:6774012  
A:Contents: myeloma protein T11  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>  
A>Note: Trp-156 is at or near the complement-binding site  
R:Comell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A>Title: The amino acid sequences of the three heavy chain constant region domains of a l  
A:Reference number: A90752; MUID:80001357; PMID:113060  
A:Contents: myeloma protein 21e  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24, 'E', 26-57, 'BY', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-;  
A>Note: this sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin ge  
A:Reference number: A93132; MUID:80114419; PMID:118920  
A:Contents: 21e  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
R:Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; 21e, revisions to residues 25, 59, 60, and 264-268  
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
ned  
R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A>Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90251; MUID:72033500; PMID:4940472  
A:Contents: annotation; myeloma protein 5a, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A>Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124; PMID:5782707  
A:Contents: annotation; 5a, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-202/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83, 140-200, 246-304/Disulfide bonds: #status experimental  
F:102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 82.3%; Score 1140; DB 1; Length 326;  
Best Local Similarity 91.3%; Pred. No. 3.6e-79;  
Matches 211; Conservative 9; Mismatches 7; Indels 4; Gaps 2;

QY 1 EPKSCDKHTHTPCPCAPAPELLGSPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 60  
DB 99 EPKCCVE--CPPCAPP-VAGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 154  
QY 61 NWYVDGVEVNAKTKPREEQYNSTYRVVSVLTVLDHQMILNGKEYKCKVSNKALPAPIEKT 120  
DB 155 KMYVDGVEVNAKTKPREEQYNSTYRVVSVLTVLDHQMILNGKEYKCKVSNKALPAPIEKT 214  
QY 121 ISKAKGPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNQGENNYKTTTP 180

Db 215 ISKTKGQPREPQYVTLPPSEEMTKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTP 274  
QY 181 PVLDSGSGFFLYSKLTVDKSRMOQGNVFCSCVHHEALHNHYTKSLSLSPG 231  
Db 275 PMLDSGSEFFLYSKLTVDKSRMOQGNVFCSCVHHEALHNHYTKSLSLSPG 325

## RESULT 9

G4HU  
Ig gamma-4 chain C region - human  
C/Species: Homo sapiens (man)  
C/Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 09-Jul-2004  
C/Accession: A90933; A02049; A02150  
R/Bilison, U.; Buxbaum, J.; Hood, L.  
DNA 1, 11-18, 1981

A/Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A/Reference number: A90933; MID:83157104; PMID:6299662

A/Accession: A90933

A/Molecule type: DNA

A/Residues: 1-327 <BL>

A/Cross-references: UNIPROT:P01861

A/Note: the sequence was determined from the germline gene

R/Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A/Title: Human immunoglobulin subclassess. Partial amino acid sequence of the constant

A/Reference number: A90249; MID:70207560; PMID:4192659

A/Accession: A90249

A/Molecule type: protein

A/Residues: 1-30;81-326 <PIN>

C/Genetics:

A/Gene: GDB:IGHG4

A/Cross-references: GDB:119340; OMIM:147130

A/Map position: 14q32.33-14q32.33

A/Intons: 99/1; 111/1; 221/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F/20-85/Domain: immunoglobulin homology <IML>

F/99-110/Region: hinge

F/134-203/Domain: immunoglobulin homology <IM2>

F/240-307/Domain: immunoglobulin homology <IM3>

F/14/Diulfide bonds: interchain (to light chain) #status experimental

F/27-83,141-201,247-305/Diulfide bonds: #status predicted

F/106,109/Diulfide bonds: interchain (to heavy chain) #status experimental

F/177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 81.6%; Score 1130; DB 1; Length 327;

Best Local Similarity 93.7%; Pred. No. 2.1e-78;

Matches 207; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 11 CPKCPAPBLIGBSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENYVDGEVH 70

Db 106 CPKCPAPBLIGBSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKENYVDGEVH 165

QY 71 NAKTKREBOYNTYRVVSVLTLDQMLNGKEYKCKVSKALPAPIEKTISKAKGPRE 130

Db 166 NAKTKREBOYNTYRVVSVLTLDQMLNGKEYKCKVSKALPAPIEKTISKAKGPRE 225

QY 131 PQYVYTPPSRDELTKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTPVLDSDGSPF 190

Db 226 PQYVYTPPSRDELTKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTPVLDSDGSPF 285

QY 191 LYSKLTVDKSRMOQGNVFCSCVHHEALHNHYTKSLSLSPG 231

Db 286 LYSKLTVDKSRMOQGNVFCSCVHHEALHNHYTKSLSLSPG 326

RESULT 10

G3MSM

Ig gamma-3 chain C region, membrane-bound form - mouse

C/Species: Mus musculus (house mouse)

C/Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text\_change 09-Jul-2004

C/Accession: B02159; A02158

R/Honjo, T.; Obata, M.; Yamawaki, K.; Katoaka, Y.; Katoaka, T.; Kawakami, T.; Takahashi, N.;

Cell 18, 559-568, 1979

A/Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain

A/Reference number: A02159; MID:80045036; PMID:115553

A/Accession: B02159

A/Molecule type: DNA

A/Residues: 1-393 <HON>

A/Cross-references: UNIPROT:P01869; GB:J00453

C/Date: 13-Aug-1986 #sequence revision 31-Mar-1991 #text\_change 09-Jul-2004  
C/Accession: A02156; A02155  
R/Mel, J.A.; Word, C.J.; Rimm, D.; Der-Balan, G.P.; Martinez, H.M.; Tucker, P.W.; Blactr  
EMBO J. 3; 12041-2046, 1984  
A/Title: Structure analysis of the murine IgG3 constant region gene.

A/Reference number: A02156; MID:85027161; PMID:6092053

A/Accession: A02156

A/Molecule type: DNA

A/Residues: 1-398 <REL>

A/Cross-references: UNIPROT:P03987; GB:J00451; MID:9194392; PIDN:ABS9655.1; PID:9194433

A/Note: the sequence was determined from the germline gene

R/Komatsu, M.; Clayton, L.; Rogers, J.; Robertson, S.; Kettman, J.; Wall, R.

Nucleic Acids Res. 11, 6775-6785, 1983

A/Title: The structure of the mouse immunoglobulin in gamma-3 membrane gene segment.

A/Reference number: A02155; MID:84041483; PMID:6114258

A/Accession: A02155

A/Molecule type: DNA

A/Residues: 328-332, 'G', 334-341, 'Q', 343-387, 'F', 389-398 <KON>

A/Cross-references: GB:K00688

A/Note: the sequence was determined from the germline gene

C/Genetics: 97/1, 113/1, 223/1, 328/1, 371/3

A/Intons: 97/1, 113/1, 223/1, 328/1, 371/3

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)

chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into 1a

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin

F/19-83/Domain: immunoglobulin homology <IM1>

F/97-112/Region: hinge

F/136-205/Domain: immunoglobulin homology <IM2>

F/242-309/Domain: immunoglobulin homology <IM3>

F/346-362/Domain: transmembrane #status predicted <TM>

F/363-398/Domain: intracellular #status predicted <INT>

F/179,322/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.8%; Score 938.5; DB 1; Length 398;

Best Local Similarity 68.4%; Pred. No. 9e-64;

Matches 167; Conservative 36; Mismatches 38; Indels 3; Gaps 1;

QY 12 PR---CPAPBLIGBSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVH 68

Db 106 PRSSCPBPNTLIGBSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGEVH 165

QY 69 VNAKTKREBOYNTYRVVSVLTLDQMLNGKEYKCKVSKALPAPIEKTISKAKGPRE 128

Db 166 VNAKTKREBOYNTYRVVSVLTLDQMLNGKEYKCKVSKALPAPIEKTISKAKGPRE 225

QY 129 REPQVYTPPSRDELTKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTPVLDSDGSPF 188

Db 226 REPQVYTPPSRDELTKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTPVLDSDGSPF 285

QY 189 FPIYSKLTVDKSRMOQGNVFCSCVHHEALHNHYTKSLSLSPG 248

Db 286 FPIYSKLTVDKSRMOQGNVFCSCVHHEALHNHYTKSLSLSPG 345

QY 249 LMTT 252

Db 346 LMTT 349

RESULT 11

G1MSM

Ig gamma-1 chain C region, membrane-bound form - mouse

C/Species: Mus musculus (house mouse)

C/Date: 17-Dec-1982 #sequence revision 31-Mar-1991 #text\_change 09-Jul-2004

C/Accession: B02159; A02158

R/Honjo, T.; Obata, M.; Yamawaki, K.; Katoaka, Y.; Katoaka, T.; Kawakami, T.; Takahashi, N.;

Cell 18, 559-568, 1979

A/Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain

A/Reference number: A02159; MID:80045036; PMID:115553

A/Accession: B02159

A/Molecule type: DNA

A/Residues: 1-393 <HON>

A/Cross-references: UNIPROT:P01869; GB:J00453



A:Cross-references: UNIPROT:P01865; GB:J00471  
 A:Note: the sequence was determined from the germline gene  
 R:Yamawaki-Karaoaka, Y.; Miyata, T.; Honjo, T.  
 Nucleic Acids Res. 9, 1365-1381, 1981  
 A:Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and env  
 A:Reference number: A32657; MUID:81198976; PMID:6262729  
 A:Accession: B32657  
 A:Molecule type: DNA  
 A:Residues: 1-329; K; <Y>A2  
 R:Hall, B.; Milcarek, C.  
 Mol. Immunol. 26, 819-826, 1989  
 A:Title: Sequence and polyadenylation site determination of the murine immunoglobulin gamma  
 A:Reference number: 157809; MUID:90097953; PMID:2513486  
 A:Accession: 157809  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 373-399 <RES>  
 A:Cross-references: GB:M35032; NID:9194478; PIDN:AAA37919.1; PID:9387217  
 C:Comment: The sequence of residues 1-328 was assumed to be identical with the correspond  
 C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma  
 hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit  
 C:Genetics: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1  
 A:Functions: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1  
 C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kap  
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotrimer; immunoglob  
 F:137-202/Domain: immunoglobulin homology <IMM>  
 F:346-363/Domain: transmembrane #status predicted <TM>  
 F:364-399/Domain: intracellular #status predicted <INT>  
 F:180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.3%; Score 905; DB 1; Length 399;  
 Best Local Similarity 66.8%; Pred. No. 3.1e-61;

Matches 163; Conservative 31; Mismatches 48; Indels 2; Gaps 1;

QY 11 CPPEBELLGSPVFLPPPKDPTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 68  
 DB 107 CPCKCPANLGGSPVFLPPPKDPTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 166  
 QY 69 VHNATKPREBOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 128  
 DB 167 VHTAQOTREHEDNSTLRVVSALPIQHODWMSGEKFCVKNNDLPAPIERITISKESGV 226  
 QY 129 REBOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDG 188  
 DB 227 RHPQVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDG 286  
 QY 189 PFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGQLDETCAADGDEL 248  
 DB 287 YFMYSKLTARBEKKNVBRNSVCSVHVEGLHNHYTQKSLSLSPGQLDETCAADGDEL 346  
 QY 249 LMTT 252  
 DB 347 LMTT 350

RESULT 14

147160  
 Ig gamma 2b chain constant region - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C:Accession: 147160  
 R:Kackovic, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
 A:Reference number: 147158; MUID:95015845; PMID:7930579  
 A:Accession: 147160  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-328 <KAC>  
 A:Cross-references: EMBL:U03760; NID:9433125; PIDN:AAA52218.1; PID:9433126  
 C:Genetics:

A:Gene: IgG2b  
 C:Superfamily: immunoglobulin C region; immunoglobulin homology  
 F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 901.5; DB 2; Length 328;  
 Best Local Similarity 73.1%; Pred. No. 4.5e-61;  
 Matches 163; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

QY 11 CPPEBELLGSPVFLPPPKDPTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 70  
 DB 106 CPICPACB-SPGSPVFLPPPKDPTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 164  
 QY 71 NATKPREBOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 130  
 DB 165 TAQTRKEQFNSTYRVSVLTPLQHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 224  
 QY 131 POVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDG 188  
 DB 225 POVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDG 284  
 QY 189 PFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 231  
 DB 285 YFLYSKFSVDKASWQGGIFQCAVMHEALHNHYTQKSLSKTPG 327

RESULT 15

147159  
 Ig gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C:Accession: 147159

R:Kackovic, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: 147158; MUID:95015845; PMID:7930579

A:Accession: 147159

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124

C:Genetics:

A:Gene: IgG2a

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 901.5; DB 2; Length 328;  
 Best Local Similarity 73.1%; Pred. No. 4.5e-61;

Matches 163; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

QY 11 CPPEBELLGSPVFLPPPKDPTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 70  
 DB 106 CPICPACB-SPGSPVFLPPPKDPTLMISRTPEVTCVVDVSHDEPEKFMVYDGEV 164  
 QY 71 NATKPREBOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 130  
 DB 165 TAQTRKEQFNSTYRVSVLTPLQHODWLNKGEYKCKVSNKALPAPIEKTISKAKGP 224  
 QY 131 POVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDG 188  
 DB 225 POVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLDSDG 284  
 QY 189 PFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPG 231  
 DB 285 YFLYSKFSVDKASWQGGIFQCAVMHEALHNHYTQKSLSKTPG 327

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 Job time : 20.6798 secs

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